



OIPE

RAW SEQUENCE LISTING

DATE: 06/16/2004

PATENT APPLICATION: US/10/055,536

TIME: 11:23:52

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1 <110> APPLICANT: DUTTA, Sukanta K.
 2 BISWAS, Biswajit
 3 VEMULAPALLI, Ramesh
 4 <120> TITLE OF INVENTION: A SIZE-VARIABLE STRAIN-SPECIFIC PROTECTIVE ANTIGEN FOR
 5 POTOMAC HORSE FEVER
 6 <130> FILE REFERENCE: 8172-9016
 7 <140> CURRENT APPLICATION NUMBER: US/10/055,536
 8 <141> CURRENT FILING DATE: 2002-01-23
 9 <150> PRIOR APPLICATION NUMBER: US/09/157,257
 10 <151> PRIOR FILING DATE: 1998-09-18
 11 <150> PRIOR APPLICATION NUMBER: 60/059,252
 12 <151> PRIOR FILING DATE: 1997-09-18
 13 <160> NUMBER OF SEQ ID NOS: 48
 14 <170> SOFTWARE: PatentIn Ver. 2.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 33
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Artificial Sequence
 20 <220> FEATURE:
 21 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
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 23 <400> SEQUENCE: 1
 24 cataaaattt ctaagacgaa ggatccctat gtc 33
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 29 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
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 40 <220> FEATURE:
 41 <221> NAME/KEY: CDS
 42 <222> LOCATION: (175)..(2721)
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 46 ttcataacaa aggactatcc tccttgcata aaatttctaa gacgaaaaat ccct atg 177

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55	act	caa	gta	ata	aaa	ggc	gag	gga	aag	aca	gaa	tta	aaa	gac	ata	ctt	321
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67	gaa	aaa	ttc	aag	gag	ctt	ttt	gga	agc	aat	ggg	aag	gac	ata	ctg	aaa	513
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78				150				155				160					
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80	Thr	Asp	Ser	Asn	Ala	Lys	Glu	Ile	Leu	Thr	Asn	Glu	Val	Ala	Lys	Glu	
81			165				170				175						
82	gta	cta	aaa	tcc	gat	aaa	ttc	aag	gag	gca	ata	act	ggc	gat	ggg	aag	753
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85	gac	gca	cta	aaa	gag	ata	ctt	act	tgt	gat	aaa	ttt	aaa	gag	gct	gta	801
86	Asp	Ala	Leu	Lys	Glu	Ile	Leu	Thr	Cys	Asp	Lys	Phe	Lys	Glu	Ala	Val	
87		195				200				205							
88	aca	ggc	aat	ggg	aaa	gac	ata	cta	aaa	ggg	ata	ctt	aca	gat	agc	act	849
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92	Gly	Lys	Phe	Lys	Glu	Leu	Ile	Glu	Ser	Thr	Ser	Lys	Asp	Ile	Leu	Lys	
93				230				235				240					
94	gag	ata	ctt	aca	gat	aat	acc	ggg	aac	ttt	aaa	ggc	ctt	ata	gaa	agc	945
95	Glu	Ile	Leu	Thr	Asp	Asn	Thr	Gly	Asn	Phe	Lys	Gly	Leu	Ile	Glu	Ser	

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98	Thr Gly Lys Glu Lys Val Lys Glu Leu Leu Ile Asp Gly Lys Phe Lys							
99		260		265		270		
100	gac ctg ttt act gat gca aca aaa gcc ggt tat gta aaa gaa ata ctc							1041
101	Asp Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu							
102		275		280		285		
103	acg aac gat aca gct aag gaa gta ctt aca gat caa aca gca aag gag							1089
104	Thr Asn Asp Thr Ala Lys Glu Val Leu Thr Asp Gln Thr Ala Lys Glu							
105		290		295		300		305
106	gtc cta aaa gat agt aca gct aaa gac ata tta aag gac aca aac gca							1137
107	Val Leu Lys Asp Ser Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn Ala							
108			310		315		320	
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110	Ala Ala Val Leu Lys Asn Ser Thr Ala Lys Glu Ile Leu Thr Asn Gln							
111			325		330		335	
112	acc gct aaa gaa gtg ctt aca gat ggt aca tcc aaa gaa gta cta aaa							1233
113	Thr Ala Lys Glu Val Leu Thr Asp Gly Thr Ser Lys Glu Val Leu Lys							
114		340		345		350		
115	gag ata ctt act tgt gat aaa ttt aaa gag gca gta aca gga gat ggt							1281
116	Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asp Gly							
117		355		360		365		
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119	Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys							
120		370		375		380		385
121	gaa ctt ata gaa agt act ggt aaa gac ata ctg aaa gac att ctt aca							1377
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125	Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Val Leu Val Lys Asn							
126		405		410		415		
127	aag cta aaa gag att ctt aca gat aac acc ggt aac ttc aaa ggg ctt							1473
128	Lys Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu							
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130	gta gaa ggc gcc ggg aag gat gaa gca aaa gca gta ctt act gac gag							1521
131	Val Glu Gly Ala Gly Lys Asp Glu Ala Lys Ala Val Leu Thr Asp Glu							
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134	Lys Phe Lys Gly Leu Phe Asp Asp Lys Thr Ile Ala Gly Tyr Val Lys							
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137	Glu Ile Leu Thr Ser Glu Lys Phe Lys Lys Leu Phe Glu Ser Ala Gly							
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139	aag act aaa gta aaa gaa ctc ctc att gat gag aag ttt caa aaa tta							1665
140	Lys Thr Lys Val Lys Glu Leu Leu Ile Asp Glu Lys Phe Gln Lys Leu							
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142	ttt gag gat gac acg aaa gcc agt cat gta aaa gaa ata ctc acg aac							1713
143	Phe Glu Asp Asp Thr Lys Ala Ser His Val Lys Glu Ile Leu Thr Asn							
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149	Lys	Asp	Ser	Thr	Ala	Lys	Glu	Ile	Leu	Lys	Asp	Thr	Asn	Ala	Ala	Ala	
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151	cta	cta	aaa	gac	agc	aca	gca	aaa	gag	gta	cta	aaa	tcc	gat	aaa	ttt	1857
152	Leu	Leu	Lys	Asp	Ser	Thr	Ala	Lys	Glu	Val	Leu	Lys	Ser	Asp	Lys	Phe	
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158	Thr	Cys	Asp	Lys	Phe	Lys	Glu	Ala	Val	Thr	Gly	Asn	Gly	Lys	Asp	Ile	
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160	cta	aaa	ggg	ata	ctt	aca	gat	agc	act	ggg	aaa	ttt	aaa	gag	cta	ata	2001
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173	Thr	Ala	Gly	Tyr	Val	Lys	Glu	Ile	Leu	Thr	Ser	Asp	Lys	Phe	Lys	Glu	
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181	cta	aag	gat	ggg	aca	gct	aaa	gac	ata	tta	aag	gac	aca	aac	gca	cgt	2337
182	Leu	Lys	Asp	Gly	Thr	Ala	Lys	Asp	Ile	Leu	Lys	Asp	Thr	Asn	Ala	Arg	
183				710								715				720	
184	gcg	cta	cta	aaa	gac	agc	aca	gcc	aaa	gaa	gta	cta	aaa	tgc	gat	aaa	2385
185	Ala	Leu	Leu	Lys	Asp	Ser	Thr	Ala	Lys	Glu	Val	Leu	Lys	Cys	Asp	Lys	
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187	ttt	aag	gaa	gca	ata	aca	ggg	gcc	ggg	aaa	gat	gag	cta	aaa	tac	ata	2433
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190	ctc	act	aat	agc	gag	ttt	aaa	agc	tta	ttt	cat	agc	aaa	gat	agc	gct	2481
191	Leu	Thr	Asn	Ser	Glu	Phe	Lys	Ser	Leu	Phe	His	Ser	Lys	Asp	Ser	Ala	
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193	gaa	gct	ggt	aaa	gca	ata	ttt	acc	cac	aat	aag	ttt	aaa	gaa	cta	ctt	2529

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197   Glu His Ala Arg Thr Thr Gln Thr Ile Arg Arg Arg Phe Ala Asn Ala
198                               790                               795                               800
199   tta gat caa cta aaa gcg cta att acc tgt ggc agc ggt gat cat gca   2625
200   Leu Asp Gln Leu Lys Ala Leu Ile Thr Cys Gly Ser Gly Asp His Ala
201                               805                               810                               815
202   aca aaa cta caa gcc ttt gga agt gca cta tgc acc aaa aag aag gag   2673
203   Thr Lys Leu Gln Ala Phe Gly Ser Ala Leu Cys Thr Lys Lys Lys Glu
204                               820                               825                               830
205   ttg tgc agt aat ttt agc tgt gca aac tgc agt agt aca aca act gca   2721
206   Leu Cys Ser Asn Phe Ser Cys Ala Asn Cys Ser Ser Thr Thr Thr Ala
207   835                               840                               845
208   taattacgta gcgctagggtg ggggtaattt acccccacct agctagaatc acacgggggaa 2781
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213 <212> TYPE: PRT
214 <213> ORGANISM: Ehrlichia risticii
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219                               20                               25                               30
220   Phe Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile
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222   Leu Thr Asp Asn Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Ala Gly
223   50                               55                               60
224   Lys Asp Ile Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys
225   65                               70                               75                               80
226   Gly Leu Ile Glu Gly Asn Gly Lys Thr Glu Ala Lys Glu Val Arg Thr
227   85                               90                               95
228   Asn Glu Lys Phe Lys Glu Leu Phe Gly Ser Asn Gly Lys Asp Ile Leu
229   100                              105                              110
230   Lys Asp Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu
231   115                              120                              125
232   Ser Ala Ala Lys Gly Lys Leu Lys Asp Leu Leu Ile Asp Glu Lys Phe
233   130                              135                              140
234   Gln Lys Leu Phe Glu Asp Glu Thr Lys Ala Gly Arg Val Lys Glu Ile
235   145                              150                              155                              160
236   Leu Thr Asp Ser Asn Ala Lys Glu Ile Leu Thr Asn Glu Val Ala Lys
237   165                              170                              175
238   Glu Val Leu Lys Ser Asp Lys Phe Lys Glu Ala Ile Thr Gly Asp Gly
239   180                              185                              190
240   Lys Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala
241   195                              200                              205
242   Val Thr Gly Asn Gly Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser
243   210                              215                              220

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

Seq#:17

VERIFICATION SUMMARY

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ORGANISM:Artificial Sequence

L:775 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence

L:775 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:775